

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,340  
Source: PCT  
Date Processed by STIC: 4-13-05

**ENTERED**



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/530,340

DATE: 04/13/2005  
TIME: 09:40:13

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF4\04132005\J530340.raw

3 <110> APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
4 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
5 HUMAN SERVICES  
6 Tsai, Robert Y.L.  
7 McKay, Ronald D.G.  
9 <120> TITLE OF INVENTION: METHODS FOR CONTROLLING PROLIFERATION OF CELLS  
11 <130> FILE REFERENCE: 4239-66642  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/530,340  
C--> 13 <141> CURRENT FILING DATE: 2005-04-01  
13 <150> PRIOR APPLICATION NUMBER: PCT/US03/31321  
14 <151> PRIOR FILING DATE: 2003-10-01  
16 <150> PRIOR APPLICATION NUMBER: 60/442,005  
17 <151> PRIOR FILING DATE: 2003-01-22  
19 <150> PRIOR APPLICATION NUMBER: 60/415,867  
20 <151> PRIOR FILING DATE: 2002-10-02  
22 <160> NUMBER OF SEQ ID NOS: 14  
24 <170> SOFTWARE: PatentIn version 3.2  
26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 1810  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Rattus rattus  
32 <220> FEATURE:  
33 <221> NAME/KEY: misc\_feature  
34 <222> LOCATION: (1705)..(1705)  
35 <223> OTHER INFORMATION: n is a, c, g, or t  
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40 cccaaagttaa agaaagcaag taaaacgtatg acctgtcata acgcgtataa aatccagaaa 120  
42 aagggttcgag aacatcatcg aaaattaagg aaggaagcta aaaagcgggg tcacaagaag 180  
44 cctaagaagg acccaggagt tccaaatagt gctccctta aagaggctct tcttcgtgaa 240  
46 gctgagctaa gaaaaacagca gcttgaagaa ctaaaacagc agcagaaaact tgacaggcaa 300  
48 aaagaacaag aacgaaaaag aaaacttcaa attagccctg atgatgagca atctaatgtg 360  
50 gaaactcagg aggaatctga tgagcccaaa ataaagaaaag ctaaatcagg caaacagaat 420  
52 ccaaagaagt tacattgtca ggaacttaaa aaggtgattg aagcctcaga cattgtgtta 480  
54 gaagtttgg atgccagaga tcctcttgg tgcaggtgtc ctcaagtaga agaagctgtt 540  
56 atccaaagtg gatgtaaaaa actagtactt gtattaaata agtcagatct agtacaaaaa 600  
58 gagaatctag agaactggct aacttacttg aataaggaat tgccaaacagt ggtgttcaaa 660  
60 gcctcaacaa acttaaagaa cagaaagaag acattcaaga taaagaagaa agttgttcca 720  
62 ttccaaagta aactctgctg tggcaaggaa gcactgtgga agctccttgg aggtttcag 780  
64 cagtcctgtg gaaaaggagt tcaggttgg a gtgggtgg tcccaaatgt gggaaaaagc 840  
66 agcatcatta atagttaaa acaagaaaagg atttgcagtg ttggagttc catgggactt 900  
68 acaaggagta tgcagattgt ccctttagac aaacagatca caatcataga tagtccgtgc 960  
70 ttcattatct caccttgtaa ctccccctgct gcacttgccc tccgaagtcc agcaagtatt 1020

(P5,6)

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72	gaagttctaa	gaccattgga	ggctgccagt	gccatcctgt	ctcaggctga	tagtcaacag	1080									
74	gtgggttaa	aatatactgt	cccggggtat	aaggattctc	tggattttt	tactaaactt	1140									
76	gctcagagaa	gaggtctgca	ccaaaaaggt	ggaagccaa	atgtcgaaag	tgctgctaag	1200									
78	ctgctatgg	ctgagtgac	aggtgcctca	ttaggtact	actgccatcc	ccctgcattcc	1260									
80	tggaaatcatt	ctcctcattt	taatgagaat	attacagcaa	tcatgaagag	gggcatttaat	1320									
82	ctagaagaac	tagaaaaaa	taatgcacac	agcatacaag	tcctcaaggg	ccctcattta	1380									
84	actaataaaaa	tcctttccg	gtcttcgggc	ctgacaaatg	gaataactaga	agaaaaaggac	1440									
86	atccccgaag	agtccacaaa	acagacagaa	gaccaacagg	atggtgatga	tcaagaacat	1500									
88	gttactggtg	aaaaaaatgc	agagatctca	gatgtgactc	ctgtagaaga	gaccaggag	1560									
90	atgtcacctg	ggcaatcaac	agcaagtaaa	ccatctgaca	gatccttat	cttggataaa	1620									
92	atgagtgaag	aagacgatgc	ctatgacttt	accacagatt	atatatagcc	ttctaaatgt	1680									
W--> 94	tcaagtgtgc	tctgtacagt	gttntagat	tgcttgta	tgatataaaag	tgttaatctt	1740									
96	gtgaatatgt	atcatgttt	aaattaaaaaa	caaaataaaaa	agtgtttgta	taaaaaaaaaaa	1800									
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102	<211> LENGTH: 538															
103	<212> TYPE: PRT															
104	<213> ORGANISM: Rattus rattus															
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112	Lys	Arg	Tyr	Lys	Ile	Gln	Lys	Lys	Val	Arg	Glu	His	His	Arg	Lys	Leu
113					20				25			30				
116	Arg	Lys	Glu	Ala	Lys	Lys	Arg	Gly	His	Lys	Pro	Lys	Lys	Asp	Pro	
117					35				40			45				
120	Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
121					50				55			60				
124	Glu	Leu	Arg	Lys	Gln	Gln	Leu	Glu	Glu	Leu	Lys	Gln	Gln	Lys	Leu	
125	65				70				75			80				
128	Asp	Arg	Gln	Lys	Glu	Gln	Glu	Arg	Lys	Arg	Lys	Leu	Glu	Ile	Ser	Pro
129					85				90			95				
132	Asp	Asp	Glu	Gln	Ser	Asn	Val	Glu	Thr	Gln	Glu	Glu	Ser	Asp	Glu	Pro
133					100				105			110				
136	Lys	Ile	Lys	Lys	Ala	Lys	Ser	Gly	Lys	Gln	Asn	Pro	Lys	Lys	Leu	His
137					115				120			125				
140	Cys	Gln	Glu	Leu	Lys	Lys	Val	Ile	Glu	Ala	Ser	Asp	Ile	Val	Leu	Glu
141					130				135			140				
144	Val	Leu	Asp	Ala	Arg	Asp	Pro	Leu	Gly	Cys	Arg	Cys	Pro	Gln	Val	Glu
145	145				150				155			160				
148	Glu	Ala	Val	Ile	Gln	Ser	Gly	Cys	Lys	Lys	Leu	Val	Leu	Val	Leu	Asn
149					165				170			175				
152	Lys	Ser	Asp	Leu	Val	Pro	Lys	Glu	Asn	Leu	Glu	Asn	Trp	Leu	Thr	Tyr
153					180				185			190				
156	Leu	Asn	Lys	Glu	Leu	Pro	Thr	Val	Val	Phe	Lys	Ala	Ser	Thr	Asn	Leu
157					195				200			205				
160	Lys	Asn	Arg	Lys	Lys	Thr	Phe	Lys	Ile	Lys	Lys	Val	Val	Pro	Phe	
161					210				215			220				
164	Gln	Ser	Lys	Leu	Cys	Cys	Gly	Lys	Glu	Ala	Leu	Trp	Lys	Leu	Leu	Gly
165	225				230				235			240				

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168 Gly Phe Gln Gln Ser Cys Gly Lys Gly Val Gln Val Gly Val Val Gly  
169 245 250 255  
172 Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu Lys Gln Glu  
173 260 265 270  
176 Arg Ile Cys Ser Val Gly Val Ser Met Gly Leu Thr Arg Ser Met Gln  
177 275 280 285  
180 Ile Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Cys Phe  
181 290 295 300  
184 Ile Ile Ser Pro Cys Asn Ser Pro Ala Ala Leu Ala Leu Arg Ser Pro  
185 305 310 315 320  
188 Ala Ser Ile Glu Val Leu Arg Pro Leu Glu Ala Ala Ser Ala Ile Leu  
189 325 330 335  
192 Ser Gln Ala Asp Ser Gln Gln Val Val Leu Lys Tyr Thr Val Pro Gly  
193 340 345 350  
196 Tyr Lys Asp Ser Leu Asp Phe Phe Thr Lys Leu Ala Gln Arg Arg Gly  
197 355 360 365  
200 Leu His Gln Lys Gly Gly Ser Pro Asn Val Glu Ser Ala Ala Lys Leu  
201 370 375 380  
204 Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Gly Tyr Tyr Cys His Pro  
205 385 390 395 400  
208 Pro Ala Ser Trp Asn His Ser Pro His Phe Asn Glu Asn Ile Thr Ala  
209 405 410 415  
212 Ile Met Lys Arg Gly Phe Asn Leu Glu Glu Leu Glu Lys Asn Asn Ala  
213 420 425 430  
216 His Ser Ile Gln Val Leu Lys Gly Pro His Leu Thr Asn Lys Ile Leu  
217 435 440 445  
220 Phe Arg Ser Ser Gly Leu Thr Asn Gly Ile Leu Glu Glu Lys Asp Ile  
221 450 455 460  
224 Pro Glu Glu Ser Pro Lys Gln Thr Glu Asp Gln Gln Asp Gly Asp Asp  
225 465 470 475 480  
228 Gln Glu His Val Thr Gly Glu Lys Asn Ala Glu Ile Ser Asp Val Thr  
229 485 490 495  
232 Pro Val Glu Glu Thr Arg Glu Met Ser Pro Gly Gln Ser Thr Ala Ser  
233 500 505 510  
236 Lys Pro Ser Asp Arg Ser Phe Ile Leu Asp Lys Met Ser Glu Glu Asp  
237 515 520 525  
240 Asp Ala Tyr Asp Phe Thr Thr Asp Tyr Ile  
241 530 535  
244 <210> SEQ ID NO: 3  
245 <211> LENGTH: 1770  
246 <212> TYPE: DNA  
247 <213> ORGANISM: Mus musculus  
249 <400> SEQUENCE: 3  
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252 gtgatcccgaa gacccctct gctcctgaag cgtccgcggc caggatgaag aggcctaagt 120  
254 taaagaaagc gagtaaacgt atgacctgcc ataagcgata taaaattcaa aaaaaggtcc 180  
256 gagaacatca tcgaaaatta aggaaggaag ctaaaaaacg gggtcacaag aagccttagga 240  
258 aggacccagg tggccaaat agtgctccct ttaaagaggc tcttcttcgt gaagctgaac 300  
260 taaggaaaca gcagcttcaa gaactaaaaac agcagcagaa acttgatagg caaaaagagc 360

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266	agttacattt	ccaggaactt	aaaaaggtga	ttgaagcctc	agacattgt	ttagaagt	540
268	tggatgccag	agatcctt	ggttgcaggt	gtcctcagat	agaaga	agact gttatccaga	600
270	gtgggagtaa	gaagctgata	cttgttattaa	ataagtctga	tctagtacca	aaggagaatt	660
272	tggagaactg	gctaaattat	ttgaataaaag	aattgccaac	cgtggtgttc	aaagcctcaa	720
274	caaacttaaa	gaacagaaaag	acattcaaga	taaaaaagaa	gaaagtgtt	ccattccaaa	780
276	gaaaaatctg	ctgtggcaag	gaagccctt	ggaagcttct	tggagat	ttt cagcagtcc	840
278	gtggaaagga	tattcaagtt	ggagtgattt	gttcccaaa	tgtggggaaa	agoagtgtca	900
280	ttaatagctt	aaaacaagaa	tggatttgca	atgttggat	ttccatggga	cttacaagga	960
282	gcatgcagat	tgtcccttta	gacaaggcaga	tcacaatcat	agacagtcca	tgccatatt	1020
284	tctcacctt	taactcccc	actgcactt	cccttcggag	tccagca	agc attgaggaac	1080
286	taagaccgct	ggaggctgcc	agtccattc	tgtctcaggc	tgataatgaa	caggtgggt	1140
288	taaaatatac	tgtccctgag	tataaggatt	ctctgcattt	ttttactaaa	cttgctcaa	1200
290	gaagaggtct	gcacccaaaa	ggttggaaagcc	caaatgttga	aagtgtct	ct aagctgggt	1260
292	ggtctgagtg	gacaggtgcc	tcatttaggtt	actattgca	tccccc	tgc tccctggaaatc	1320
294	attctctgca	ttttatgag	aatattgcag	cagtcatgaa	gaagggc	ttt aatctagaag	1380
296	aactagaaaa	gaataatgca	cacagcatac	aagtccctaa	gggc	ccctcat ttaactaata	1440
298	gaatccttt	tcggcttcg	ggcctgacaa	atggaatact	agacgagaag	gacatagtcg	1500
300	aagagaccag	ggagctgtca	cctgagcaat	caacagcagg	taagccatct	gacgggtcg	1560
302	ctgccttgg	tagagcgagt	caagaggat	aaacctatga	cttcaccaca	gattatata	1620
304	aaccgccaca	cactaacgtg	ctctctgtac	gctgtgtat	ttagtgtat	g atataaactg	1680
306	tacatctt	gt aaatatgtat	catgttataa	attcaaaata	aaatacaagt	atttgcttgc	1740
308	aaaaaaaaaa	aaaaaaaaact	cgactctaga				1770

311 <210> SEQ ID NO: 4

312 <211> LENGTH: 538

313 <212> TYPE: PRT

314 <213> ORGANISM: Mus musculus

316 <400> SEQUENCE: 4

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322	Lys	Arg	Tyr	Lys	Ile	Gln	Lys	Lys	Val	Arg	Glu	His	His	Arg	Lys	Leu
323					20				25				30			
326	Arg	Lys	Glu	Ala	Lys	Lys	Arg	Gly	His	Lys	Lys	Pro	Arg	Lys	Asp	Pro
327					35				40				45			
330	Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
331					50				55				60			
334	Glu	Leu	Arg	Lys	Gln	Gln	Leu	Glu	Glu	Leu	Lys	Gln	Gln	Gln	Lys	Leu
335					65				70				75			80
338	Asp	Arg	Gln	Lys	Glu	Gln	Glu	Arg	Lys	Arg	Lys	Leu	Glu	Val	Ser	Pro
339									85				90			95
342	Gly	Asp	Glu	Gln	Ser	Asn	Val	Glu	Thr	Arg	Glu	Glu	Ser	Asp	Glu	Pro
343									100				105			110
346	Lys	Arg	Lys	Lys	Ala	Lys	Ala	Gly	Lys	Gln	Asn	Pro	Lys	Lys	Leu	His
347									115				120			125
350	Cys	Gln	Glu	Leu	Lys	Lys	Val	Ile	Glu	Ala	Ser	Asp	Ile	Val	Leu	Glu
351									130				135			140
354	Val	Leu	Asp	Ala	Arg	Asp	Pro	Leu	Gly	Cys	Arg	Cys	Pro	Gln	Ile	Glu
355									145				150			160
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358 Glu Ala Val Ile Gln Ser Gly Ser Lys Lys Leu Ile Leu Val Leu Asn  
359 165 170 175  
362 Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Asn Trp Leu Asn Tyr  
363 180 185 190  
366 Leu Asn Lys Glu Leu Pro Thr Val Val Phe Lys Ala Ser Thr Asn Leu  
367 195 200 205  
370 Lys Asn Arg Lys Thr Phe Lys Ile Lys Lys Lys Val Val Pro Phe  
371 210 215 220  
374 Gln Ser Lys Ile Cys Cys Gly Lys Glu Ala Leu Trp Lys Leu Leu Gly  
375 225 230 235 240  
378 Asp Phe Gln Gln Ser Cys Gly Lys Asp Ile Gln Val Gly Val Ile Gly  
379 245 250 255  
382 Phe Pro Asn Val Gly Lys Ser Ser Val Ile Asn Ser Leu Lys Gln Glu  
383 260 265 270  
386 Trp Ile Cys Asn Val Gly Ile Ser Met Gly Leu Thr Arg Ser Met Gln  
387 275 280 285  
390 Ile Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Cys Leu  
391 290 295 300  
394 Ile Ile Ser Pro Cys Asn Ser Pro Thr Ala Leu Ala Leu Arg Ser Pro  
395 305 310 315 320  
398 Ala Ser Ile Glu Glu Leu Arg Pro Leu Glu Ala Ala Ser Ala Ile Leu  
399 325 330 335  
402 Ser Gln Ala Asp Asn Glu Gln Val Val Leu Lys Tyr Thr Val Pro Glu  
403 340 345 350  
406 Tyr Lys Asp Ser Leu His Phe Phe Thr Lys Leu Ala Gln Arg Arg Gly  
407 355 360 365  
410 Leu His Gln Lys Gly Ser Pro Asn Val Glu Ser Ala Ala Lys Leu  
411 370 375 380  
414 Val Trp Ser Glu Trp Thr Gly Ala Ser Leu Gly Tyr Tyr Cys His Pro  
415 385 390 395 400  
418 Pro Ala Ser Trp Asn His Ser Leu His Phe Asn Glu Asn Ile Ala Ala  
419 405 410 415  
422 Val Met Lys Lys Gly Phe Asn Leu Glu Glu Leu Glu Lys Asn Asn Ala  
423 420 425 430  
426 His Ser Ile Gln Val Leu Lys Gly Pro His Leu Thr Asn Arg Ile Leu  
427 435 440 445  
430 Phe Arg Ser Ser Gly Leu Thr Asn Gly Ile Leu Asp Glu Lys Asp Ile  
431 450 455 460  
434 Val Glu Glu Ser Pro Ser Gln Thr Glu Asp Gln Gln Asp Ala Asp Asp  
435 465 470 475 480  
438 Gln Glu Asn Gly Ser Gly Glu Arg Asn Ala Glu Ile Ser Asp Val Ala  
439 485 490 495  
442 Pro Val Glu Glu Thr Arg Glu Leu Ser Pro Glu Gln Ser Thr Ala Gly  
443 500 505 510  
446 Lys Pro Ser Asp Gly Ser Ser Ala Leu Asp Arg Ala Ser Gln Glu Asp  
447 515 520 525  
450 Glu Thr Tyr Asp Phe Thr Thr Asp Tyr Ile  
451 530 535  
454 <210> SEQ ID NO: 5

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 22,23  
Seq#:8; N Pos. 22,23  
Seq#:9; N Pos. 22,23  
Seq#:10; Xaa Pos. 39,45,70,86,88,94,95,97,98,99,100,105,106,108,109,110,111  
Seq#:10; Xaa Pos. 112,113,114,115,116,117,121,126,130,143,161,165,166,170  
Seq#:10; Xaa Pos. 174,176,190,193,196,205,209,210,212,213,214,216,218,219  
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Seq#:10; Xaa Pos. 252,254,255,256,260,270,278,279,281,284,294,308,309,311  
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Seq#:10; Xaa Pos. 374,380,385,390,400,407,410,411,412,413,414,418,420,421  
Seq#:10; Xaa Pos. 422,425,438,441,442,443,449,451,455,464,465,470,473,475  
Seq#:10; Xaa Pos. 476,477,479,480,482,483,484,485,486,487,488,489,490,494  
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VERIFICATION SUMMARY  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1680  
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32  
M:341 Repeated in SeqNo=10